==
Sequence Listing was accepted.

See attached Validation Report.

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217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=4; day=4; hr=10; min=57; sec=23; ms=140;]
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Application No: 10588140   Version No: 2.0

                    Input Set:

                    Output Set:

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                       Finished: 2008-03-25 11:51:40.868
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                Total Warnings: 9
                  Total Errors: 3
        No. of SeqIDs Defined: 9
          Actual SeqID Count: 9

Error code   Error Description

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W   213   Artificial or Unknown found in <213> in SEQ ID (2)

W   213   Artificial or Unknown found in <213> in SEQ ID (3)

W   213   Artificial or Unknown found in <213> in SEQ ID (4)

W   213   Artificial or Unknown found in <213> in SEQ ID (5)

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E   257   Invalid sequence data feature in <221> in SEQ ID (8)

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W   213   Artificial or Unknown found in <213> in SEQ ID (9)

E   257   Invalid sequence data feature in <221> in SEQ ID (9)

<110> KIM, DO-MAN
      KANG, HEE-KYOUNG
      LEE, JIN-HA

<120> PROTEIN WITH ACTIVITY OF HYDROLYZING DEXTRAN, STARCH,
      MUTAN, INULIN, AND LEVAN, GENE ENCODING THE SAME, CELL
      EXPRESSING THE SAME, AND PRODUCTION METHOD THEREOF

<130> 44352-0010-00-US

<140> 10588140
<141> 2006-07-31

<150> PCT/KR05/00234
<151> 2005-01-27

<150> KR 10-2004-0006185
<151> 2004-01-30

<160> 9

<170> PatentIn Ver. 3.3

<210> 1
<211> 608
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      construct

<400> 1
Met Thr Leu Ile Tyr Val Pro Ser Ile Phe Thr Met Val Pro Ser Ile
  1   5   10   15

Thr Arg Ile Val Leu Val Asn Ile Leu Leu Ala Thr Leu Val Leu Gly
            20   25   30

Ala Ala Val Leu Pro Arg Asp Asn Arg Thr Val Cys Gly Ser Gln Leu
        35   40   45

Cys Thr Trp Trp His Asp Ser Gly Glu Ile Asn Thr Gly Thr Pro Val
    50   55   60

Gln Ala Gly Asn Val Arg Gln Ser Arg Lys Tyr Ser Val His Val Ser
 65   70   75   80

Leu Ala Asp Arg Asn Gln Phe Tyr Asp Ser Phe Val Tyr Glu Ser Ile
                85   90   95

Pro Arg Asn Gly Asn Gly Arg Ile Tyr Ser Pro Thr Asp Pro Pro Asn
            100   105   110

Ser Asn Thr Leu Asn Ser Ser Ile Asp Asp Gly Ile Ser Ile Glu Pro
        115   120   125

Ser Leu Gly Ile Asn Met Ala Trp Ser Gln Phe Glu Tyr Arg Arg Asp
        130   135   140

Val Asp Ile Lys Ile Thr Thr Ile Asp Gly Ser Ile Leu Asp Gly Pro
145   150   155   160

Leu Asp Ile Val Ile Arg Pro Thr Ser Val Lys Tyr Ser Val Lys Arg
                165   170   175

Cys Val Gly Gly Ile Ile Ile Arg Val Pro Tyr Asp Pro Asn Gly Arg
                180   185   190

Lys Phe Ser Val Glu Leu Lys Ser Asp Leu Tyr Ser Tyr Leu Ser Asp
        195   200   205

Gly Ser Gln Tyr Val Thr Ser Gly Gly Ser Val Val Gly Val Glu Pro
        210   215   220

Lys Asn Ala Leu Val Ile Phe Ala Ser Pro Phe Leu Pro Arg Asp Met
225   230   235   240

Val Pro His Met Thr Pro His Asp Thr Gln Thr Met Lys Pro Gly Pro
                245   250   255

Ile Asn Asn Gly Asp Trp Gly Ser Lys Pro Ile Leu Tyr Phe Pro Pro
                260   265   270

Gly Val Tyr Trp Met Asn Glu Asp Thr Ser Gly Asn Pro Gly Lys Leu
        275   280   285

Gly Ser Asn His Met Arg Leu Asp Pro Asn Thr Tyr Trp Val His Leu
        290   295   300

Ala Pro Gly Ala Tyr Val Lys Gly Ala Ile Glu Tyr Phe Thr Lys Gln
305   310   315   320

Asn Phe Tyr Ala Thr Gly His Gly Val Leu Ser Gly Glu Asn Tyr Val
                325   330   335

Tyr Gln Ala Asn Ala Ala Asp Asn Tyr Tyr Ala Val Lys Ser Asp Gly
                340   345   350

Thr Ser Leu Arg Met Trp Trp His Asn Asn Leu Gly Gly Gly Gln Thr
        355   360   365

Trp Phe Cys Met Gly Pro Thr Ile Asn Ala Pro Pro Phe Asn Thr Met
        370   375   380

Asp Phe Asn Gly Asn Ser Asn Ile Ser Ser Arg Ile Ser Asp Tyr Lys
385   390   395   400

Gln Val Gly Ala Tyr Phe Phe Gln Thr Asp Gly Pro Glu Ile Tyr Glu
                405   410   415

Asp Ser Val Val His Asp Val Phe Trp His Val Asn Asp Asp Ala Ile
          420   425   430

Lys Thr Tyr Tyr Ser Gly Ala Ser Ile Ser Arg Ala Thr Ile Trp Lys
          435   440   445

Cys His Asn Asp Pro Ile Ile Gln Met Gly Trp Thr Ser Arg Asn Leu
      450   455   460

Thr Gly Ile Ser Ile Asp Asn Leu His Val Ile His Thr Arg Tyr Phe
465   470   475   480

Lys Ser Glu Thr Val Val Pro Ser Ala Ile Ile Gly Ala Ser Pro Phe
              485   490   495

Tyr Ala Ser Gly Met Thr Val Asp Pro Ser Glu Ser Ile Ser Met Thr
          500   505   510

Ile Ser Asn Val Val Cys Glu Gly Leu Cys Pro Ser Leu Phe Arg Ile
          515   520   525

Thr Pro Leu Gln Ser Tyr Asn Asn Leu Val Val Lys Asn Val Ala Phe
      530   535   540

Pro Asp Gly Leu Gln Thr Asn Pro Ile Gly Ile Gly Glu Ser Ile Ile
545   550   555   560

Pro Ala Ala Ser Gly Cys Thr Met Asp Leu Glu Ile Thr Asn Trp Thr
          565   570   575

Val Lys Gly Gln Lys Val Thr Met Gln Asn Phe Gln Ser Gly Ser Leu
          580   585   590

Gly Gln Phe Asp Ile Asp Gly Ser Tyr Trp Gly Gln Trp Ser Ile Asn
          595   600   605

<210> 2
<211> 2052
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      construct

<220>
<221> CDS
<222> (42)..(1865)

<400> 2
tgggtgtgtc ccttgctctg ccaacgttgt tgattgtttt c atg aca tta atc tac   56
                                             Met Thr Leu Ile Tyr
                                               1   5

gtg cct tca ata ttt aca atg gtc ccc tca atc aca cgg att gta ctg   104
Val Pro Ser Ile Phe Thr Met Val Pro Ser Ile Thr Arg Ile Val Leu

gtt aac att ctg ttg gcg acg ttg gtt ttg gga gct gca gtc ctt cca   152
Val Asn Ile Leu Leu Ala Thr Leu Val Leu Gly Ala Ala Val Leu Pro
            25   30   35

cga gac aac aga act gtt tgc ggg agt caa ctc tgc aca tgg tgg cac   200
Arg Asp Asn Arg Thr Val Cys Gly Ser Gln Leu Cys Thr Trp Trp His
            40   45   50

gac tcc ggc gag ata aac acc ggt act cct gta cag gca gga aac gtt   248
Asp Ser Gly Glu Ile Asn Thr Gly Thr Pro Val Gln Ala Gly Asn Val
        55   60   65

cga caa tcc cga aag tac tct gtc cat gtg agc ctg gca gac cgt aac   296
Arg Gln Ser Arg Lys Tyr Ser Val His Val Ser Leu Ala Asp Arg Asn
    70   75   80   85

caa ttc tac gac tct ttc gta tat gaa tcg ata cct agg aac ggc aat   344
Gln Phe Tyr Asp Ser Phe Val Tyr Glu Ser Ile Pro Arg Asn Gly Asn
                90   95   100

ggc aga att tat tct ccc acc gac cca cct aac agc aat aca ttg aat   392
Gly Arg Ile Tyr Ser Pro Thr Asp Pro Pro Asn Ser Asn Thr Leu Asn
            105   110   115

agt agc att gac gac ggt ata tca atc gaa cca tct ctc ggc atc aac   440
Ser Ser Ile Asp Asp Gly Ile Ser Ile Glu Pro Ser Leu Gly Ile Asn
            120   125   130

atg gct tgg tcc cag ttc gaa tat aga cga gat gtc gac att aag att   488
Met Ala Trp Ser Gln Phe Glu Tyr Arg Arg Asp Val Asp Ile Lys Ile
    135   140   145

act aca atc gat ggc tca ata ttg gat ggc cct ttg gac att gtt att   536
Thr Thr Ile Asp Gly Ser Ile Leu Asp Gly Pro Leu Asp Ile Val Ile
150   155   160   165

cgg ccg act tct gtt aag tac tca gtc aaa aga tgt gtg ggt ggt atc   584
Arg Pro Thr Ser Val Lys Tyr Ser Val Lys Arg Cys Val Gly Gly Ile
            170   175   180

att att aga gtc cct tat gat ccc aat ggt cga aaa ttc tct gtt gag   632
Ile Ile Arg Val Pro Tyr Asp Pro Asn Gly Arg Lys Phe Ser Val Glu
            185   190   195

tta aag agt gac ctt tac agt tac ctc tcc gac ggt tcg caa tat gtg   680
Leu Lys Ser Asp Leu Tyr Ser Tyr Leu Ser Asp Gly Ser Gln Tyr Val
            200   205   210

acc tct gga ggg agc gtg gtt ggt gtg gag cca aaa aat gcc ctg gtg   728
Thr Ser Gly Gly Ser Val Val Gly Val Glu Pro Lys Asn Ala Leu Val
            215   220   225

atc ttt gcc agc cct ttc ttg cca cgg gat atg gtt cct cat atg aca   776
Ile Phe Ala Ser Pro Phe Leu Pro Arg Asp Met Val Pro His Met Thr
230   235   240   245

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cca cac gac acc cag aca atg aag ccg ggc cca atc aat aat ggg gac      824
Pro His Asp Thr Gln Thr Met Lys Pro Gly Pro Ile Asn Asn Gly Asp
            250                 255                 260

tgg ggt tca aag cct ata ctc tac ttc ccg cct ggc gta tac tgg atg      872
Trp Gly Ser Lys Pro Ile Leu Tyr Phe Pro Pro Gly Val Tyr Trp Met
            265                 270                 275

aac gag gat acc tct ggt aac ccc ggg aag ctc ggc tca aat cat atg      920
Asn Glu Asp Thr Ser Gly Asn Pro Gly Lys Leu Gly Ser Asn His Met
            280                 285                 290

cgg ctg gat ccc aat acc tac tgg gtc cat cta gcc cca gga gcc tat      968
Arg Leu Asp Pro Asn Thr Tyr Trp Val His Leu Ala Pro Gly Ala Tyr
            295                 300                 305

gtg aaa gga gcc att gag tat ttc acg aag caa aat ttc tat gca acg     1016
Val Lys Gly Ala Ile Glu Tyr Phe Thr Lys Gln Asn Phe Tyr Ala Thr
310                 315                 320                 325

ggt cat ggc gtt ctc tca ggt gag aac tat gtt tat cag gcc aat gca     1064
Gly His Gly Val Leu Ser Gly Glu Asn Tyr Val Tyr Gln Ala Asn Ala
            330                 335                 340

gct gat aac tac tat gcc gtc aag agt gat ggc aca agc ttg aga atg     1112
Ala Asp Asn Tyr Tyr Ala Val Lys Ser Asp Gly Thr Ser Leu Arg Met
            345                 350                 355

tgg tgg cac aac aac ctt gga ggc ggt caa aca tgg ttt tgc atg ggg     1160
Trp Trp His Asn Asn Leu Gly Gly Gly Gln Thr Trp Phe Cys Met Gly
            360                 365                 370

ccc acc att aat gca ccg ccg ttt aat acg atg gac ttc aac gga aac     1208
Pro Thr Ile Asn Ala Pro Pro Phe Asn Thr Met Asp Phe Asn Gly Asn
            375                 380                 385

tct aat att tcc agc cgg att agt gac tat aag cag gtt ggc gct tat     1256
Ser Asn Ile Ser Ser Arg Ile Ser Asp Tyr Lys Gln Val Gly Ala Tyr
390                 395                 400                 405

ttt ttc caa aca gac gga ccg gag atc tac gag gac agt gtt gtc cat     1304
Phe Phe Gln Thr Asp Gly Pro Glu Ile Tyr Glu Asp Ser Val Val His
            410                 415                 420

gac gtc ttc tgg cat gtt aat gat gat gcc atc aag aca tat tat tcc     1352
Asp Val Phe Trp His Val Asn Asp Asp Ala Ile Lys Thr Tyr Tyr Ser
            425                 430                 435

gga gct tca att tca cga gca acc atc tgg aag tgt cac aat gac ccg     1400
Gly Ala Ser Ile Ser Arg Ala Thr Ile Trp Lys Cys His Asn Asp Pro
            440                 445                 450

atc ata cag atg ggc tgg acg tca cga aat ctc acc gga atc agc att     1448
Ile Ile Gln Met Gly Trp Thr Ser Arg Asn Leu Thr Gly Ile Ser Ile
    455                 460                 465
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gat aac ctg cac gtc atc cac acg aga tat ttc aaa tct gaa aca gtg      1496
Asp Asn Leu His Val Ile His Thr Arg Tyr Phe Lys Ser Glu Thr Val
470              475              480              485

gtt cct tca gca atc att gga gcg tct cca ttc tac gca agt gga atg      1544
Val Pro Ser Ala Ile Ile Gly Ala Ser Pro Phe Tyr Ala Ser Gly Met
            490              495              500

act gtt gat ccc agc gag tcc atc agc atg acc atc tct aac gtg gtg      1592
Thr Val Asp Pro Ser Glu Ser Ile Ser Met Thr Ile Ser Asn Val Val
            505              510              515

tgt gag ggt cta tgc ccc tca ctg ttc cgt atc act ccg ctt cag agc      1640
Cys Glu Gly Leu Cys Pro Ser Leu Phe Arg Ile Thr Pro Leu Gln Ser
        520              525              530

tac aac aac ctt gtt gtc aag aac gtg gcc ttt ccc gat gga ctg cag      1688
Tyr Asn Asn Leu Val Val Lys Asn Val Ala Phe Pro Asp Gly Leu Gln
    535              540              545

aca aat cca atc gga ata gga gag agc att ata cca gca gct tcc ggc      1736
Thr Asn Pro Ile Gly Ile Gly Glu Ser Ile Ile Pro Ala Ala Ser Gly
550              555              560              565

tgt aca atg gac ttg gaa atc aca aac tgg acc gtc aaa gga caa aaa      1784
Cys Thr Met Asp Leu Glu Ile Thr Asn Trp Thr Val Lys Gly Gln Lys
            570              575              580

gtc acc atg caa aac ttt cag tcc ggg tca ctt ggc cag ttc gat atc      1832
Val Thr Met Gln Asn Phe Gln Ser Gly Ser Leu Gly Gln Phe Asp Ile
            585              590              595

gat ggt tca tac tgg ggt caa tgg tcc ata aac taaagctatt cccattcacc 1885
Asp Gly Ser Tyr Trp Gly Gln Trp Ser Ile Asn
        600              605

tgagtatttt cgtgggttca atgagttctt gttactgatg gggcccttgc tagtggtaaa 1945

agtagaggga cttgtcctcg ccgggcgcca aggaagttca tgtcttctag ttgaatagta 2005

tttgtttctt ctctctcgtt aaaaaaaaaa aaaaaaaaaa aaaaaaa              2052


<210> 3
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 3
gtcccttgag ctcccaac                                              18


<210> 4
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<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 4
tcaactagaa ttcatgaact tcc   23

<210> 5
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 5
gagagagaga gagagagaga actagtctcg agtttttttt tttttttttt   50

<210> 6
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 6
acctggcaya grdmm   15

<210> 7
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 7
gsykccsacc tgcttrta   18

<210> 8
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (5)
<223> Asp or Asn

<220>
<221> MOD_RES
<222> (6)
<223> Asn, Ser or Thr

<400> 8
Thr Trp Trp His Xaa Xaa
  1   5

<210> 9
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

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<221> MOD_RES
<222> (6)
<223> Ser or Ala

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Tyr Lys Gln Val Gly Xaa
  1   5